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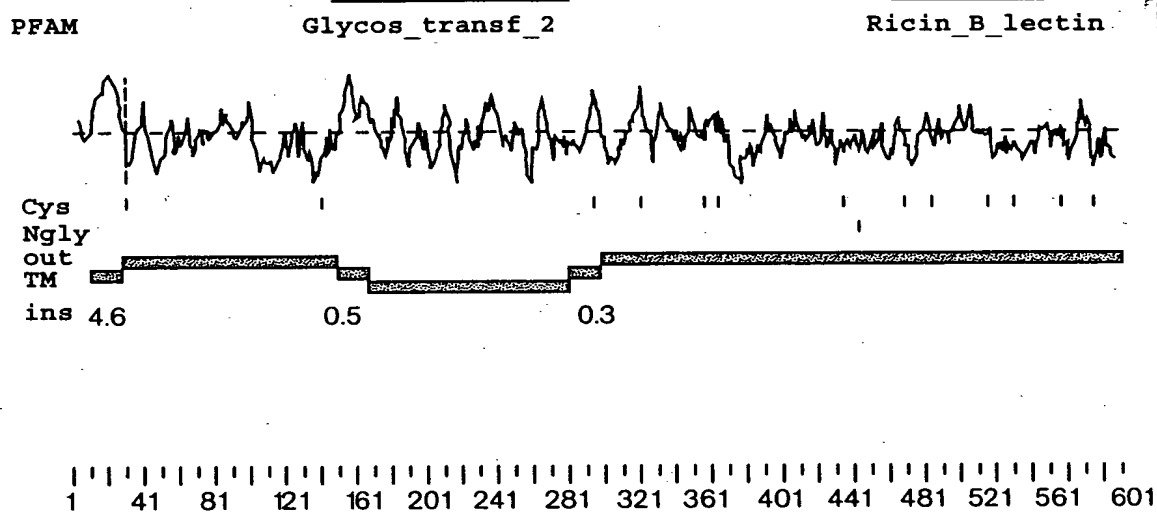


Fig. 1

Glycos\_transf\_2: domain 1 of 1, from 154 to 336: score 55.7, E = 1e-12  
 \*->sivIptYNeeadyLeelleSvlaqs.tledieiivDDgSetDetve  
 s+v + Ne+++ +++ ++Sv + + + e+i vDD+S + e++  
 47174 154 SVVFIFVNEALSVILRSVHSVNHtpSQLLKEVILVDDNSDNVELKF 200  
 iaedylderikeenpriiivirleensqGpaaArnkgirratGdsdyIlf  
 ++ y+ ++ +p + ++r++++ G +Ar +g ++at ++ f  
 47174 201 NLDQYV---NKRYPLVKIVRNSRRE-GLIRARLQGWKAATAP--VVGf 243  
 LDaDdiftpdkleklidyaeatdaavvlgaida.....yeyaegesnlr  
 +Da+++f ++ e+++++++ ++ +vl+aid + +++e +++ + ++  
 47174 244 FDAHVEFNTGWAEPALSRIREDRRRIVLPAIDNikystFEVQQYANA-AH 292  
 iaradterslfagllrktgrltgglelsfeigsnaiyrreafeelf<-\*  
 ++++ ++ ++ +++ +r g+ ++ +++++ + ++ +++e+f  
 47174 293 GYNWGLWCMYIIPPQDWLDR--GDESAPIRTPAMIGCSFVVDREYF 336

Fig. 2

Alignments of top-scoring domains:

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ricin_3: domain 1 of 1, from 465 to 595: score 32.5, E =9.8e-06
      *>rgyflliiggntglCLdvngnsesksdGnpvglwdChgggnQlWkltY
      +g ++ + ++ CLd +++++ + +l++Chg ++Ql +++
47174  465  YGEVRNSK-ASAYCLDQGAEDGD-----RAILYPCHGMSSQLVRYS- 504
      nesdgairi.....nsdlCLtvng...tvtylsCdgtckgndnQk.
      dg + ++ +++ + +CL +g+++ tl++C++ + + Q+
47174  505  --ADGLQLGplgstafIPDSKCLVDDGtgrMPTLKKCEDV--ARPTQRl 550
      WevnkdgcirnpknskkgvdsglcLdvkdgn.....kvqlwtcngsdap
      W + ++g i+++ +g cL+v +++ + + +++ c+g
47174  551  WDFtQSGPIVSR-----ATGRCLEVEMSKdanfglRLVVQRCSG----- 589
      nQkWife<-*
      QkW ++
47174  590  -QKWMIR 595

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Fig. 3

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>2308 p99.2 (23) PAGT(3) // N-ACETYL GALACTOSAMINYLTRANSFERASE TRANSFERASE  
POLYPEPTIDE ACETYL GALACTOSAMINYLTRANSFERASE UDP-GALNAC:POLYPEPTIDE  
GLYCOSYLTRANSFERASE PROTEIN-UDP PROTEIN-UDP N-  
LENGTH = 172

Score = 423 (154.0 bits), Expect = 4.7e-40, P = 4.7e-40  
Identities = 77/151 (50%), Positives = 104/151 (68%)

Query: 312 RGDESAPIRTPAMIGCSFVVDREYFGDIGLLDPGMEVYGGENVELGMRVWQC GGSMEVLP 371  
R D + PIR+P M G F +++EYF ++G DPGM+++GGEN+EL RVWQCGG +E++P  
Sbjct: 14 RKDPTDPIRSPTMAGGLFAINKEYFEELGTYDPGMDIWGGENLELSFRVWQCGRLEIVP 73

Query: 372 CS RVAHIERTRKPYNN DIDYYAK----RNALRAAEVWMDDFKSHVYMAWNIPMSNPGVDF 427  
CS V H+ R R PY K RN +R AEVWMD+K + Y + P + DF  
Sbjct: 74 CSHVGHVFRKRSPYTFPGKSGKDVISRNTVRVAEVWMDDYKEYFYK--HNPQARKVRDF 131

Query: 428 GDVSERLALRQRLKCRSFKWYLENVYPEMRV 458  
GD+SER LR++L+C+SFKWYLENVYP++ V  
Sbjct: 132 GDISERKELREKLQCKSFKWYLENVYPDLV 162

Fig. 4